

RESULT 6
US-10-367-057-53
; Sequence 53, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 53
; LENGTH: 958
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-53

Query Match 100.0%; Score 82; DB 5; Length 958;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RQSLLGSRRGRSSSLSLAK 18
Db 104 RQSLLGSRRGRSSSLSLAK 121

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	1	"20050100554"	US-PGPUB; USPAT	OR	ON	2006/10/20 14:02
L2	1	L1 and antibod\$	US-PGPUB; USPAT	OR	ON	2006/10/20 14:04
L3	4	GEF-H1 near antibod\$	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/10/20 15:09
L4	4	(GEF-H1 or ARHGEF2) near antibod\$	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/10/20 15:11
L5	22	(GEF-H1 or ARHGEF2) and antibod\$	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/10/20 15:12
L6	27	GEF-H1 or ARHGEF2	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	ON	2006/10/20 15:13

d his

(FILE 'HOME' ENTERED AT 17:05:10 ON 20 OCT 2006)

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 17:05:29 ON 20 OCT 2006

L1 9 S (GEF-H1 OR GEFH1 OR ARHGEF2) AND ANTIBOD?
L2 80 S GEF-H1 OR GEFH1 OR ARHGEF2
L3 9 DUP REM L1 (0 DUPLICATES REMOVED)
L4 41 DUP REM L2 (39 DUPLICATES REMOVED)
L5 97 S SMEAL T R/AU OR CALLOW M G/AU OR JALLAL B/AU
L6 44 DUP REM L5 (53 DUPLICATES REMOVED)
L7 1 S L2 AND L6

=>

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OM protein - protein search, using sw model

Run on: September 19, 2006, 23:22:28 ; Search time 182 Seconds
(without alignments)
45.812 Million cell updates/sec

Title: US-10-611-671-4
Perfect score: 82
Sequence: 1 RQSLLGSRRGRSSLSLAK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	82	100.0	18	4	US-10-611-671-4	Sequence 4, Appli
2	82	100.0	19	4	US-10-611-671-8	Sequence 8, Appli
3	82	100.0	19	4	US-10-611-671-9	Sequence 9, Appli

4	82	100.0	46	4	US-10-611-671-49	Sequence 49, Appl
5	82	100.0	920	4	US-10-611-671-2	Sequence 2, Appli
6	82	100.0	958	5	US-10-367-057-53	Sequence 53, Appl
7	82	100.0	994	5	US-10-723-860-2066	Sequence 2066, Ap
8	54	65.9	18	4	US-10-611-671-47	Sequence 47, Appl
9	50	61.0	85	4	US-10-425-115-245626	Sequence 245626,
10	45	54.9	69	4	US-10-425-115-225403	Sequence 225403,
11	43	52.4	140	4	US-10-425-115-333843	Sequence 333843,
12	43	52.4	264	6	US-11-096-568A-25037	Sequence 25037, A
13	43	52.4	285	6	US-11-096-568A-25036	Sequence 25036, A
14	43	52.4	2360	4	US-10-437-963-187801	Sequence 187801,
15	42	51.2	69	4	US-10-437-963-129723	Sequence 129723,
16	42	51.2	681	4	US-10-437-963-195028	Sequence 195028,
17	41	50.0	53	3	US-09-864-408A-7878	Sequence 7878, Ap
18	41	50.0	163	4	US-10-437-963-161912	Sequence 161912,
19	41	50.0	188	5	US-10-467-657-3200	Sequence 3200, Ap
20	41	50.0	197	4	US-10-437-963-165251	Sequence 165251,
21	41	50.0	205	4	US-10-335-977-5888	Sequence 5888, Ap
22	41	50.0	297	4	US-10-425-115-351232	Sequence 351232,
23	41	50.0	303	4	US-10-335-977-5889	Sequence 5889, Ap
24	41	50.0	310	4	US-10-335-977-5890	Sequence 5890, Ap
25	41	50.0	361	4	US-10-425-114-51048	Sequence 51048, A
26	41	50.0	695	4	US-10-156-761-13358	Sequence 13358, A
27	41	50.0	796	3	US-09-801-368-30	Sequence 30, Appl
28	41	50.0	797	6	US-11-097-143-21042	Sequence 21042, A
29	41	50.0	1522	4	US-10-437-963-175194	Sequence 175194,
30	40	48.8	18	4	US-10-211-088-35	Sequence 35, Appl
31	40	48.8	96	4	US-10-425-115-311936	Sequence 311936,
32	40	48.8	122	4	US-10-425-115-306244	Sequence 306244,
33	40	48.8	123	4	US-10-437-963-163757	Sequence 163757,
34	40	48.8	139	6	US-11-096-568A-1451	Sequence 1451, Ap
35	40	48.8	150	4	US-10-425-115-268317	Sequence 268317,
36	40	48.8	160	4	US-10-744-149-14	Sequence 14, Appl
37	40	48.8	160	5	US-10-744-620-14	Sequence 14, Appl
38	40	48.8	160	6	US-11-096-568A-1450	Sequence 1450, Ap
39	40	48.8	210	6	US-11-096-568A-23933	Sequence 23933, A
40	40	48.8	244	4	US-10-437-963-168353	Sequence 168353,
41	40	48.8	247	6	US-11-096-568A-23932	Sequence 23932, A
42	40	48.8	248	4	US-10-425-115-300754	Sequence 300754,
43	40	48.8	249	4	US-10-425-114-57244	Sequence 57244, A
44	40	48.8	262	4	US-10-180-375-136	Sequence 136, App
45	40	48.8	262	4	US-10-183-687-266	Sequence 266, App
46	40	48.8	262	4	US-10-425-115-233343	Sequence 233343,
47	40	48.8	270	4	US-10-425-114-69441	Sequence 69441, A
48	40	48.8	563	4	US-10-639-720A-2	Sequence 2, Appli
49	40	48.8	563	4	US-10-704-332-7	Sequence 7, Appli
50	40	48.8	563	4	US-10-704-332-9	Sequence 9, Appli
51	40	48.8	563	4	US-10-704-332-11	Sequence 11, Appl
52	40	48.8	563	4	US-10-704-332-14	Sequence 14, Appl
53	40	48.8	564	4	US-10-704-332-18	Sequence 18, Appl
54	40	48.8	698	4	US-10-437-963-156597	Sequence 156597,
55	40	48.8	712	4	US-10-437-963-112121	Sequence 112121,
56	40	48.8	746	4	US-10-425-114-64987	Sequence 64987, A
57	39.5	48.2	1494	4	US-10-437-963-194014	Sequence 194014,
58	39	47.6	78	4	US-10-767-701-47752	Sequence 47752, A
59	39	47.6	84	4	US-10-425-115-249302	Sequence 249302,
60	39	47.6	86	4	US-10-425-115-256239	Sequence 256239,
61	39	47.6	86	4	US-10-425-115-356540	Sequence 356540,
62	39	47.6	89	4	US-10-437-963-188270	Sequence 188270,
63	39	47.6	103	4	US-10-425-115-205500	Sequence 205500,
64	39	47.6	107	4	US-10-425-115-292377	Sequence 292377,

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OM protein - protein search, using sw model

Run on: September 19, 2006, 23:23:43 ; Search time 32 Seconds
(without alignments)
39.739 Million cell updates/sec

Title: US-10-611-671-4
Perfect score: 82
Sequence: 1 RQSLLGSRGRSSLSLAK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 256596 seqs, 70647373 residues

Total number of hits satisfying chosen parameters: 256596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:
 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query
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No.	Score	Match Length	DB	ID	Description
1	40	48.8	139	6 US-10-953-349-39556	Sequence 39556, A
2	40	48.8	160	6 US-10-953-349-39555	Sequence 39555, A
3	40	48.8	210	7 US-11-056-355B-17985	Sequence 17985, A
4	40	48.8	244	6 US-10-449-902-50983	Sequence 50983, A
5	40	48.8	247	7 US-11-056-355B-17984	Sequence 17984, A
6	40	48.8	540	6 US-10-449-902-45649	Sequence 45649, A
7	40	48.8	1115	7 US-11-056-355B-78536	Sequence 78536, A
8	40	48.8	1121	7 US-11-056-355B-78535	Sequence 78535, A
9	40	48.8	1181	7 US-11-056-355B-49997	Sequence 49997, A
10	40	48.8	1187	7 US-11-056-355B-49996	Sequence 49996, A
11	40	48.8	1191	7 US-11-056-355B-78534	Sequence 78534, A
12	40	48.8	1257	7 US-11-056-355B-49995	Sequence 49995, A
13	39	47.6	200	7 US-11-056-355B-65451	Sequence 65451, A
14	39	47.6	256	6 US-10-449-902-39280	Sequence 39280, A
15	39	47.6	257	6 US-10-953-349-2510	Sequence 2510, Ap
16	39	47.6	257	7 US-11-056-355B-38462	Sequence 38462, A
17	39	47.6	257	7 US-11-056-355B-105972	Sequence 105972,
18	39	47.6	257	7 US-11-056-355B-117211	Sequence 117211,
19	39	47.6	264	6 US-10-953-349-2509	Sequence 2509, Ap
20	39	47.6	264	7 US-11-056-355B-38461	Sequence 38461, A
21	39	47.6	264	7 US-11-056-355B-105971	Sequence 105971,
22	39	47.6	264	7 US-11-056-355B-117210	Sequence 117210,
23	39	47.6	271	6 US-10-449-902-32465	Sequence 32465, A
24	39	47.6	272	6 US-10-953-349-11616	Sequence 11616, A
25	39	47.6	299	7 US-11-056-355B-105970	Sequence 105970,
26	39	47.6	299	7 US-11-056-355B-117209	Sequence 117209,
27	39	47.6	301	6 US-10-449-902-56312	Sequence 56312, A
28	39	47.6	380	7 US-11-056-355B-20182	Sequence 20182, A
29	39	47.6	391	7 US-11-056-355B-20181	Sequence 20181, A
30	39	47.6	432	6 US-10-449-902-48478	Sequence 48478, A
31	38	46.3	258	6 US-10-953-349-26872	Sequence 26872, A
32	38	46.3	277	7 US-11-056-355B-82606	Sequence 82606, A
33	38	46.3	403	7 US-11-330-403-2526	Sequence 2526, Ap
34	38	46.3	403	7 US-11-330-403-16284	Sequence 16284, A
35	38	46.3	433	6 US-10-953-349-26871	Sequence 26871, A
36	38	46.3	789	6 US-10-449-902-46564	Sequence 46564, A
37	38	46.3	789	6 US-10-449-902-48999	Sequence 48999, A
38	38	46.3	1536	7 US-11-330-403-1325	Sequence 1325, Ap
39	37	45.1	72	6 US-10-449-902-44527	Sequence 44527, A
40	37	45.1	113	7 US-11-056-355B-13716	Sequence 13716, A
41	37	45.1	114	7 US-11-293-697-4571	Sequence 4571, Ap
42	37	45.1	151	7 US-11-056-355B-13713	Sequence 13713, A
43	37	45.1	392	7 US-11-330-403-7739	Sequence 7739, Ap
44	37	45.1	402	7 US-11-330-403-6636	Sequence 6636, Ap
45	37	45.1	406	7 US-11-330-403-5333	Sequence 5333, Ap
46	37	45.1	434	7 US-11-221-332-94	Sequence 94, Appl
47	37	45.1	602	7 US-11-056-355B-88014	Sequence 88014, A
48	37	45.1	604	7 US-11-056-355B-88013	Sequence 88013, A
49	37	45.1	639	7 US-11-056-355B-88012	Sequence 88012, A
50	37	45.1	644	7 US-11-056-355B-71272	Sequence 71272, A
51	37	45.1	679	7 US-11-056-355B-71271	Sequence 71271, A
52	37	45.1	686	7 US-11-030-653-22	Sequence 22, Appl
53	37	45.1	752	7 US-11-056-355B-71270	Sequence 71270, A
54	36	43.9	134	6 US-10-449-902-51228	Sequence 51228, A
55	36	43.9	142	6 US-10-449-902-55870	Sequence 55870, A
56	36	43.9	187	6 US-10-953-349-6691	Sequence 6691, Ap
57	36	43.9	188	6 US-10-953-349-8410	Sequence 8410, Ap
58	36	43.9	197	6 US-10-953-349-6690	Sequence 6690, Ap
59	36	43.9	201	7 US-11-056-355B-24263	Sequence 24263, A

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OM protein - protein search, using sw model

Run on: September 19, 2006, 23:17:18 ; Search time 39 Seconds
(without alignments)
44.408 Million cell updates/sec

Title: US-10-611-671-4
Perfect score: 82
Sequence: 1 RQSLLGSRRGRSSLSLAK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description
No.	Score	Match	Length	DB ID	
1	75	91.5	573	2 I49342	hypothetical oncog
2	43	52.4	405	2 AI3232	replication protei
3	42	51.2	86	2 E64003	hypothetical prote
4	41	50.0	188	2 G81155	hypothetical prote
5	41	50.0	188	2 H81949	hypothetical prote
6	41	50.0	250	2 T14546	beta-fructofuranos
7	41	50.0	796	1 A32434	abaA protein - Eme
8	40	48.8	414	2 C89428	protein T08D2.7 [i]

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OM protein - protein search, using sw model

Run on: September 19, 2006, 23:13:02 ; Search time 296 Seconds
(without alignments)
56.251 Million cell updates/sec

Title: US-10-611-671-4

Perfect score: 82

Sequence: 1 RQSLLGSRGRSSLSSLAK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	% Match Length DB ID				Description
		1	2	3	4	
1	82	100.0	893	1	ARHG2_HUMAN	Q92974 homo sapien
2	82	100.0	958	2	Q9H023_HUMAN	Q9h023 homo sapien
3	82	100.0	959	2	Q8WUG4_HUMAN	Q8wug4 homo sapien
4	82	100.0	964	2	Q865S2_CANFA	Q865s2 canis famil

5	82	100.0	985	2	Q8TDA3_HUMAN	Q8tda3 homo sapien
6	82	100.0	986	2	Q5VY92_HUMAN	Q5vy92 homo sapien
7	82	100.0	986	2	Q865S3_CANFA	Q865s3 canis famil
8	82	100.0	987	2	Q5VY93_HUMAN	Q5vy93 homo sapien
9	75	91.5	596	1	ARHG2_MOUSE	Q60875 mus musculu
10	75	91.5	637	2	Q3TYZ4_MOUSE	Q3tyz4 mus musculu
11	75	91.5	956	2	Q3TBI4_MOUSE	Q3tbi4 mus musculu
12	75	91.5	958	2	Q3TJ16_MOUSE	Q3tj16 mus musculu
13	75	91.5	985	2	Q5FVC2_RAT	Q5fvc2 rattus norv
14	75	91.5	985	2	Q8CHE1_MOUSE	Q8chel mus musculu
15	75	91.5	985	2	Q923E0_MOUSE	Q923e0 mus musculu
16	75	91.5	985	2	Q9ESG7_MOUSE	Q9esg7 mus musculu
17	72	87.8	98	2	Q9W736_XENLA	Q9w736 xenopus lae
18	72	87.8	967	2	Q6INN2_XENLA	Q6inn2 xenopus lae
19	72	87.8	976	2	Q6AX47_XENLA	Q6ax47 xenopus lae
20	69	84.1	978	2	Q6NY14_XENTR	Q6ny14 xenopus tro
21	69	84.1	1129	2	Q4SWE0_TETNG	Q4swe0 tetraodon n
22	62	75.6	279	2	Q4RAP6_TETNG	Q4rap6 tetraodon n
23	49	59.8	187	2	Q5DGZ3_SCHJA	Q5dgz3 schistosoma
24	48	58.5	483	1	CIMA_METAC	Q8tjj1 methanosarc
25	48	58.5	483	1	CIMA_METMA	P58966 methanosarc
26	48	58.5	483	2	Q46FZ1_METBA	Q46fz1 methanosarc
27	45	54.9	268	2	Q2LR09_9DELT	Q2lr09 syntrophus
28	44	53.7	56	2	Q7UQY8_RHOBA	Q7uqy8 rhodopirell
29	44	53.7	162	2	Q396A1_BURS3	Q396a1 burkholderi
30	44	53.7	401	2	Q3STK5_NITWN	Q3stk5 nitrobacter
31	44	53.7	442	2	Q6FVR1_CANGA	Q6fvr1 candida gla
32	44	53.7	485	2	Q41Q17_METBU	Q41ql7 methanococc
33	43.5	53.0	694	2	Q56JK9_APIME	Q56jk9 apis mellif
34	43	52.4	158	2	Q54BV1_DICDI	Q54bv1 dictyosteli
35	43	52.4	164	2	Q72A69_DESVH	Q72a69 desulfovibr
36	43	52.4	405	2	O66165_9RHIZ	O66165 agrobacteri
37	43	52.4	405	2	Q8U691_AGRT5	Q8u691 agrobacteri
38	43	52.4	411	2	Q7D2P0_AGRT5	Q7d2p0 agrobacteri
39	43	52.4	483	2	Q8ZT56_PYRAE	Q8zt56 pyrobaculum
40	43	52.4	656	2	Q2JUF7_9CYAN	Q2juf7 cyanobacter
41	43	52.4	758	2	Q6BZ53_DEBHA	Q6bz53 debaryomyce
42	43	52.4	1399	2	Q4PBD7_USTMA	Q4pb7 ustilago ma
43	43	52.4	2013	2	Q4UAG2_THEAN	Q4uag2 theileria a
44	43	52.4	2825	2	Q6EUI5_ORYSA	Q6eui5 oryza sativ
45	42.5	51.8	290	2	Q5B6D9_EMENI	Q5b6d9 aspergillus
46	42	51.2	76	2	Q6K5X0_ORYSA	Q6k5x0 oryza sativ
47	42	51.2	86	1	Y173_HAEIN	P43960 haemophilus
48	42	51.2	262	2	Q3AY18_SYN9	Q3ay18 synechococc
49	42	51.2	285	2	Q7U6M3_SYNPX	Q7u6m3 synechococc
50	42	51.2	335	2	Q4RN31_TETNG	Q4rn31 tetraodon n
51	42	51.2	373	2	Q6LRV3_PHOPR	Q6lrv3 photobacter
52	42	51.2	399	2	Q8GVC7_PHYIN	Q8gvc7 phytophthor
53	42	51.2	411	2	Q3W7X0_9ACTO	Q3w7x0 frankia sp.
54	42	51.2	606	2	Q7S6R5_NEUCR	Q7s6r5 neurospora
55	42	51.2	1203	2	Q4P9D2_USTMA	Q4p9d2 ustilago ma
56	42	51.2	1572	2	Q4D1E2_TRYCR	Q4d1e2 trypanosoma
57	42	51.2	1572	2	Q4DUN0_TRYCR	Q4dun0 trypanosoma
58	41.5	50.6	189	2	Q3G1G5_9DELT	Q3g1g5 pelobacter
59	41	50.0	63	2	Q8VNR2_ECOLI	Q8vnr2 escherichia
60	41	50.0	106	2	Q8KL53_RHIET	Q8kl53 rhizobium e
61	41	50.0	188	2	Q5F9K2_NEIG1	Q5f9k2 neisseria g
62	41	50.0	188	2	Q9JV31_NEIMA	Q9jv31 neisseria m
63	41	50.0	188	2	Q9K019_NEIMB	Q9k019 neisseria m
64	41	50.0	228	2	Q4TGG5_TETNG	Q4tgg5 tetraodon n
65	41	50.0	250	2	Q42646_BETVU	Q42646 beta vulgar

SCORE Search Results Details for Application 10611671 and Search Result us-10-611-671-4.i

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OM protein - protein search, using sw model

Run on: September 19, 2006, 23:22:18 ; Search time 51 Seconds
(without alignments)
30.893 Million cell updates/sec

Title: US-10-611-671-4
Perfect score: 82
Sequence: 1 RQSLLGSRRGRSSLSLAK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	%				Description
		Match	Length	DB	ID	
1	43	52.4	534	2	US-09-252-991A-32086	Sequence 32086, A
2	42	51.2	774	2	US-09-252-991A-29669	Sequence 29669, A

SCORE Search Results Details for Application 10611671 and Search Result us-10-611-671- 4.rag.

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OM protein - protein search, using sw model

Run on: September 19, 2006, 23:12:23 ; Search time 197 Seconds
(without alignments)
41.776 Million cell updates/sec

Title: US-10-611-671-4

Perfect score: 82

Sequence: 1 RQSLLGSRRGRSSLSSLAK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	82	100.0	18	8	ADI34764	Adi34764 Human GEF
2	82	100.0	19	8	ADI34769	Adi34769 GEF-H1S K
3	82	100.0	19	8	ADI34768	Adi34768 GEF-H1S K
4	82	100.0	920	8	ADI34762	Adi34762 Human GEF
5	82	100.0	948	8	ABM83436	Abm83436 Human dia
6	82	100.0	958	7	ADF09552	Adf09552 Human rho
7	82	100.0	958	8	ABM83443	Abm83443 Human dia
8	82	100.0	969	8	ABM83440	Abm83440 Human dia
9	82	100.0	969	8	ABM83439	Abm83439 Human dia
10	82	100.0	969	8	ABM83441	Abm83441 Human dia
11	82	100.0	972	8	ABM83442	Abm83442 Human dia
12	82	100.0	985	8	ADS88428	Ads88428 Human pro
13	82	100.0	994	8	ADQ19247	Adq19247 Human sof
14	82	100.0	995	8	ABM83438	Abm83438 Human dia
15	82	100.0	996	8	ABM83437	Abm83437 Human dia
16	43	52.4	79	4	AAU62434	Aau62434 Propionib
17	43	52.4	79	6	ABM58953	Abm58953 Propionib
18	43	52.4	534	7	ABO83340	Abo83340 Pseudomon
19	42	51.2	72	5	ABP09181	Abp09181 Human ORF
20	42	51.2	399	7	ABB80244	Abb80244 P. infest
21	42	51.2	774	7	ABO80923	Abo80923 Pseudomon
22	41	50.0	53	5	ABP34966	Abp34966 Human ORF
23	41	50.0	65	3	AAG57071	Aag57071 Arabidops
24	41	50.0	188	3	AYY75226	Aay75226 Neisseria
25	41	50.0	188	3	AYY75228	Aay75228 Neisseria
26	41	50.0	188	3	AYY75227	Aay75227 Neisseria
27	41	50.0	188	6	ABP78335	Abp78335 N. gonorr
28	41	50.0	188	9	AEB19124	Aeb19124 Neisseria
29	41	50.0	200	7	ABO74829	Abo74829 Pseudomon
30	41	50.0	205	2	AAW20158	Aaw20158 H. pylori
31	41	50.0	310	2	AAW20871	Aaw20871 H. pylori
32	41	50.0	361	8	ADX88384	Adx88384 Plant ful
33	41	50.0	419	7	ABO79741	Abo79741 Pseudomon
34	41	50.0	797	4	ABB64750	Abb64750 Drosophil
35	41	50.0	812	2	AAR10047	Aar10047 abaA gene
36	40	48.8	133	7	ABO77465	Abo77465 Pseudomon
37	40	48.8	160	3	AYY96218	Aay96218 Maize LEC
38	40	48.8	182	2	AYY73936	Aay73936 Human pro
39	40	48.8	249	8	ADX94580	Adx94580 Plant ful
40	40	48.8	262	6	ABR40723	Abr40723 Zea mays
41	40	48.8	262	7	ADC23631	Adc23631 Polypepti
42	40	48.8	270	8	ADY13626	Ady13626 Plant ful
43	40	48.8	563	8	ADK71105	Adk71105 Human aci
44	40	48.8	563	8	ADP43823	Adp43823 Human CB1
45	40	48.8	563	8	ADP43825	Adp43825 Human FB4
46	40	48.8	563	8	ADP43830	Adp43830 Human aci
47	40	48.8	563	8	ADP43827	Adp43827 Human SC2
48	40	48.8	564	8	ADP43834	Adp43834 Human SC2
49	40	48.8	746	8	ADY09172	Ady09172 Plant ful
50	40	48.8	769	9	ABM97417	Abm97417 M. xanthu
51	40	48.8	860	8	ADI28828	Adi28828 Human mod
52	40	48.8	908	5	ABB97232	Abb97232 Novel hum
53	40	48.8	1257	8	ADU20533	Adu20533 A. thalia
54	40	48.8	1257	8	ADU20384	Adu20384 A. thalia
55	39	47.6	18	7	ADC22186	Adc22186 Protein b
56	39	47.6	64	7	ABM89344	Abm89344 Rice abio
57	39	47.6	165	8	ADX74951	Adx74951 Plant ful